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| **Domains related with abiotic streesess** | **InterproScan** | **p value** | **Analysis** | **Function** |
| SNF1-related protein kinase regulatory subunit beta-2 | IPR030070 | 4.73904822918744e-06 | FQ | Drought, carbohydrate metabolism, glucose limitation, assimilation of nitrogen |
| Association with the SNF1 complex (ASC) domain | IPR006828 | 2.35820186485343e-05 | FQ | Glucose limitation, nutritional stress |
| ASC domain superfamily | IPR037256 | 2.35820186485343e-05 | FQ | Glucose limitation |
| Zinc/iron permease | IPR003689 | 0.000814604948648228 | FQ | Symbiotic nitrogen fixation, acquisition, distribution, homeostasis, and signaling of Zn |
| Zinc/iron permease, fungal/plant | IPR003689 | 0.000814604948648228 | FQ | Mycorrhizal interaction |
| Molybdopterin dehydrogenase, FAD-binding | IPR016166 | 0.000185413832771727 | FQ | Purine degradation and stress response |
| 2Fe-2S ferredoxin, iron-sulphur binding site | IPR006058 | 0.00029834063051467 | FQ | Photosynthesis, biosynthesis of chlorophyll, phytochrome and fatty acids, assimilation of sulphur and nitrogen |
| 2Fe-2S ferredoxin-like superfamily | IPR036010 | 5.29814156300357e-06 | FQ | Photosynthesis, biosynthesis of chlorophyll, phytochrome and fatty acids, assimilation of sulphur and nitrogen |
| CO dehydrogenase flavoprotein, C-terminal | IPR005107 | 1.63748425958808e-08 | FQ | Blue light, seedling establishment, phototropism and circadian clock regulation |
| CO dehydrogenase flavoprotein, C-terminal domain superfamily | IPR036683 | 1.63748425958808e-08 | FQ | Blue light, seedling establishment, phototropism and circadian clock regulation |
| Aldehyde oxidase/xanthine dehydrogenase, molybdopterin binding | IPR008274 | 1.63748425958808e-08 | FQ | Biosynthesis of abscisic acid and indole-3-acetic acid, freezing, drought and salinity, purine metabolism |
| NADH:ubiquinone oxidoreductase | IPR003918 | 0.00705652132531428 | FQ | Reducing nitrate to nitrite |
| NADH-quinone oxidoreductase, subunit D superfamily | IPR038290 | 0.00015710346454611 | FQ | Reducing nitrate to nitrite |
| NADH-quinone oxidoreductase, subunit D | IPR001135 | 8.57244057505102e-05 | FQ | Reducing nitrate to nitrite |
| NADH-quinone oxidoreductase chain 4 | IPR022997 | 0.00880688768728087 | FQ | Reducing nitrate to nitrite |
| DNA-binding pseudobarrel domain superfamily | IPR015300 | 0.00227701807998442/1.64679852792304e-05 | E, PS | Plant growth and development, modeling of root architecture, and development of seeds |
| Isoprenoid synthase domain superfamily | IPR008949 | 0.000190959341615375/1.64679852792304e-05 | E, PS | Carbon Partitioning Within the Cytoplasmic Pathway |
| Photosystem I PsaA/PsaB superfamily | IPR036408 | 0.000387846621742638 | E | Uses light energy to mediate electron transfer from plastocyanin to ferredoxin |
| Photosystem I PsaA/PsaB | IPR001280 | 1.18728617549622e-05 | E | Uses light energy to mediate electron transfer from plastocyanin to ferredoxin |
| Photosystem I PsaA | IPR006243 | 3.06849009137618e-05 | E | Uses light energy to mediate electron transfer from plastocyanin to ferredoxin |
| Photosystem I PsaA/PsaB, conserved site | IPR020586 | 0.00880688768728087 | E | Uses light energy to mediate electron transfer from plastocyanin to ferredoxin |
| F-box domain | IPR001810 | 1.04835685971051e-07/1.1556973950776e-07 | E, PS | Floral transition as well as panicle and seed development and floral transition as well as panicle and seed development |
| F-box-like domain superfamily | IPR036047 | 1.11431588301656e-09/2.09398570489204e-12 | E, PS | Floral transition as well as panicle and seed development and floral transition as well as panicle and seed development |
| F-box associated interaction domain | IPR017451 | 1.03216044469383e-21/1.78796851106414e-28 | E, PS | Floral transition as well as panicle and seed development and floral transition as well as panicle and seed development |
| Transcription factor, MADS-box superfamily | IPR036879 | 1.21271003369215e-35/4.23506692043568e-25 | E, PS | Floral development |
| Transcription factor, MADS-box | IPR002100 | 3.38729039856136e-35/4.23506692043568e-25 | E, PS | Floral development |
| F-box associated domain, type 1 | IPR006527 | 1.07559236634639e-05/1.10923398190436e-05 | E, PS | Floral development |
| ALOG domain | IPR006936 | 0.00194921350000857 | E | Key developmental regulators |
| ALOG family | IPR040222 | 0.00540851156133388 | E | Key developmental regulators |
| START-like domain superfamily | IPR023393 | 0.000387846621742638 | E | Response to drought, salt, wound and heat stress, stress response |
| Galactose oxidase/kelch, beta-propeller | IPR011043 | 0.00995866392790922/0.00234048616451657 | E, PS | Stress responses induced under Fe deficiency in the roots |
| HAT, C-terminal dimerisation domain | IPR008906 | 3.9617311897511e-05 | E | Abiotic and biotic stress |
| Protein EMBRYONIC FLOWER 1 | IPR034583 | 0.00227104562540973 | E | Controls leaves development, shoot architecture and flowering by delaying both the vegetative to reproductive transition and flower initiation |
| Protein NUCLEAR FUSION DEFECTIVE 6 | IPR033251 | 0.000353460646875219 | E | Nuclear fusion in sexual reproduction |
| Double-stranded RNA-binding protein | IPR031147 | 0.00705652132531428 | E | Plant hormone signaling |
| Ulp1 protease family, C-terminal catalytic domain | IPR003653 | 2.29378084276168e-07 | E | Salt stress signaling |
| Domain of unknown function DUF4283 | IPR025558 | 1.55983230739787e-34/2.96781657689533e-14 | E, PS | Cell wall biology, vasculature patterning and abiotic/biotic stress response |
| Chlorophyll a/b binding domain superfamily | IPR023329 | 0.00663846128936449 | PS | Light receptor that captures and delivers excitation energy to photosystems I and II |
| Chlorophyll A-B binding protein, plant | IPR001344 | 0.00663846128936449 | PS | Light receptor that captures and delivers excitation energy to photosystems I and II |
| Reverse transcriptase zinc-binding domain | IPR026960 | 4.86159448263943e-05 | PS | Leaf senescence |